Length of CAE-final1: 2373 bp; Listed from: 1 to: 2373;
Translated from: 1 to: 2371 (whole region);
Genetic Code used: Universal; Fri, Mar 4, 2005 10:36AM

```
Frame 1 Met Ala Asn Ser Tyr Asn Ala Tyr Val Ala Asn Gly Ser Gln Thr Ala Phe
        ATG GCG AAC AGC TAT AAT GCT TAC GTG GCG AAC GGT TCA CAG ACC GCA TTC
                  9         18         27         36         45

Leu Val Thr Phe Glu Gln Arg Val Phe Thr Glu Ile Gln Val Tyr Leu Asn Ser Glu
CTC GTC ACG TTC GAG CAG CGC GTG TTC ACT GAG ATT CAG GTG TAC CTC AAC TCC GAA
         60         69         78         87         96        105

Leu Gln Thr Glu Gly Tyr Thr Tyr Asn Ser Val Thr Lys Gln Ile Ile Phe Asp Thr
CTC CAG ACG GAA GGG TAC ACC TAC AAC TCT GTG ACC AAA CAG ATT ATC TTC GAC ACC
        117        126        135        144        153        162

Ala Pro Leu Ala Gly Val Ile Val Arg Leu Gln Arg Tyr Thr Ser Glu Val Leu Leu
GCC CCG CTC GCC GGG GTG ATT GTC CGA CTC CAA CGC TAC ACC TCT GAG GTT CTG CTG
        174        183        192        201        210        219

Asn Lys Phe Gly Gln Asp Ala Ala Phe Thr Gly Gln Asn Leu Asp Glu Asn Phe Glu
AAC AAG TTT GGC CAA GAC GCT GCC TTC ACC GGG CAG AAC CTT GAC GAG AAC TTT GAG
        231        240        249        258        267        276

Gln Ile Leu Phe Lys Ala Glu Glu Thr Gln Glu Ala Trp Leu Ala Pro Leu Asp Arg
CAG ATT CTG TTC AAG GCT GAG GAA ACT CAG GAA GCA TGG CTC GCG CCA CTT GAC CGC
        288        297        306        315        324        333

Ala Val Arg Val Pro Asn Ser Glu Val Ser Ile Asn Ala Leu Pro Asn Val Ala Gly
GCC GTC CGT GTT CCG AAC TCC GAA GTC TCC ATC AAC GCA TTA CCG AAC GTC GCT GGC
        345        354        363        372        381        390

Arg Arg Asn Lys Ala Leu Gly Phe Asp Ser Asn Gly Gln Pro Phe Met Ile Pro Leu
CGC CGC AAC AAG GCA CTG GGC TTT GAC AGC AAT GGT CAG CCG TTC ATG ATT CCT CTG
        402        411        420        429        438        447

Val Asp Ile Pro Asp Ser Ala Leu Ala Ile Ala Leu Ala Met Ala Asp Gly Gly Lys
GTC GAT ATC CCG GAC TCC GCG CTG GCG ATT GCT CTG GCA ATG GCT GAC GGC GGT AAG
        459        468        477        486        495        504

Trp Ile Gly Thr Leu Gly Gly Gly Thr Phe Leu Asp Arg Gln Asp Thr Val Cys Leu
TGG ATT GGT ACT CTC GGC GGG GGC ACG TTC CTC GAC CGT CAG GAT ACC GTC TGC CTG
        516        525        534        543        552        561
```

FIG. 1A

```
Ser Glu Phe Thr Asn Asn Thr Gly Tyr Ala Ser Val Ala Ala Ala Val Gln Ala Cys
TCC GAG TTC ACC AAC AAC ACT GGG TAC GCC TCT GTC GCC GCT GCG GTG CAG GCT TGC
        573         582         591         600         609         618

Phe Asp Tyr Ala Lys Ala Asn Gly Lys Val Val Asp Ala Arg Gly Trp Glu Gly Thr
TTC GAC TAT GCG AAA GCC AAC GGC AAG GTC GTT GAC GCT CGC GGC TGG GAA GGT ACG
        630         639         648         657         666         675

Val Asp Ser Thr Val Leu Met Asp Gly Ile Glu Val Val Gly Gly Thr Trp His Gly
GTG GAT TCC ACT GTG CTG ATG GAC GGT ATT GAG GTC GTC GGC GGT ACG TGG CAC GGC
        687         696         705         714         723         732

Lys Ala Asp Ile Arg Leu Leu Asn ser Thr Phe Arg Asn Phe Val Ala Ser Thr Val
AAG GCT GAC ATT CGC CTG CTG AAC TCC ACC TTC CGC AAC TTC GTG GCC TCT ACT GTC
        744         753         762         771         780         789

Arg Val Ala Tyr Trp Gly Gly Glu Val Arg Ile Ala Asp Tyr Glu Phe Thr Ser Ala
CGT GTC GCC TAC TGG GGC GGC GAG GTG CGT ATT GCT GAC TAT GAG TTC ACC AGC GCA
        801         810         819         828         837         846

Pro Ser Asn Ser Lys Val Thr Ser Ile Leu Phe Gln Gly Asn Ile Ala Gly Gly Ser
CCG AGC AAC TCC AAG GTT ACG TCT ATC CTG TTC CAA GGC AAC ATC GCC GGG GGC AGC
        858         867         876         885         894         903

Tyr Val Ile Glu Asn Gly Ile His Arg Asn Gly Lys Phe Gly Ile Leu Gln Gln Gly
TAC GTC ATT GAG AAC GGT ATC CAC CGC AAT GGT AAG TTC GGT ATT CTC CAA CAG GGT
        915         924         933         942         951         960

Thr Gly Glu Ala Ile Thr Asn Gly Val Ile Arg Gly Ile Thr Met Met Asp Met Gln
ACT GGC GAG GCT ATC ACC AAC GGC GTT ATC CGT GGC ATC ACC ATG ATG GAT ATG CAG
        972         981         990         999        1008        1017

Gly Asp Gly Ile Glu Met Asn Val Ile Asn Lys His Tyr Asp Gly Gly Leu Leu Ile
GGT GAC GGT ATC GAG ATG AAC GTA ATC AAC AAG CAC TAT GAT GGT GGC CTG CTG ATT
       1029        1038        1047        1056        1065        1074

Glu Asn Ile Phe Leu Glu Asn Ile Asp Gly Thr Asn Ala Pro Ile Pro Leu Ser Asn
GAG AAC ATC TTC CTT GAG AAC ATC GAC GGC ACC AAC GCG CCT ATC CCA CTG TCC AAC
       1086        1095        1104        1113        1122        1131

Trp Gly Ile Gly Ile Gly Ile Ala Gly Gln Gly Pro Phe Gly Trp Asp Ala Ala Glu
TGG GGC ATT GGT ATC GGT ATC GCT GGT CAA GGC CCG TTC GGT TGG GAT GCT GCT GAG
       1143        1152        1161        1170        1179        1188
```

FIG. 1B

```
Thr Gln Tyr Ala Lys Asn Val Thr Val Arg Asn Val His Ala Pro Arg Gly Val Arg
ACG CAG TAT GCG AAG AAC GTC ACT GTC CGT AAC GTC CAT GCT CCG CGT GGT GTG CGT
      1200        1209        1218        1227        1236        1245

Gln Val Val His Phe Glu Val Thr Arg Asp Ser Thr Cys Glu Asn Val Val Ala Asn
CAG GTC GTC CAC TTC GAG GTT ACG CGT GAC AGC ACC TGC GAG AAC GTA GTG GCC AAC
      1257        1266        1275        1284        1293        1302

Pro Asp Leu Ser Val Ser Ile Gly Thr Gly Leu Thr Ala Ala Gly Val Ile Thr Tyr
CCT GAC CTG TCC GTC TCC ATT GGT ACT GGC CTG ACT GCC GCT GGT GTA ATC ACG TAC
      1314        1323        1332        1341        1350        1359

Gly Cys Lys Arg Met Thr Ile Asp Gly Val Val Gly Glu Pro Met Asn Thr Gly Ala
GGC TGC AAG CGC ATG ACC ATT GAC GGT GTA GTC GGT GAG CCT ATG AAC ACC GGA GCA
      1371        1380        1389        1398        1407        1416

Thr Ser Pro Asn Asp Ile Arg Ile Val Met Leu Glu Trp Gly Ala Asn Gln Ala Gly
ACC TCT CCG AAC GAT ATT CGT ATC GTG ATG TTG GAG TGG GGT GCG AAC CAA GCA GGT
      1428        1437        1446        1455        1464        1473

Ala Gly Gly Thr Pro Gly Ala Ala Cys Pro Ser Phe Asp Met Thr Val Arg Asn Val
GCT GGC GGT ACG CCG GGT GCA GCT TGC CCA TCG TTC GAC ATG ACC GTG CGT AAC GTG
      1485        1494        1503        1512        1521        1530

Gln Thr Arg Thr Gly Arg Phe Tyr Ala Gly Val Gly Ser Asp Asp Asp Asn Thr Asn
CAG ACC CGT ACC GGG CGC TTC TAT GCT GGT GTC GGC TCC GAC GAT GAC AAC ACC AAC
      1542        1551        1560        1569        1578        1587

Thr Tyr His Leu Glu Asn Ile His Cys Tyr Lys Met Thr Leu Phe Gly Val Ala Thr
ACA TAT CAC CTT GAA AAC ATT CAC TGT TAC AAG ATG ACG CTG TTT GGT GTG GCA ACT
      1599        1608        1617        1626        1635        1644

Leu Leu Asn Met Thr Asn Val Thr Gly Val Val Phe Asp Ala Val Gly Asp Asp Ser
CTG CTG AAC ATG ACC AAC GTG ACT GGT GTG GTG TTC GAC GCT GTA GGC GAT GAC TCC
      1656        1665        1674        1683        1692        1701

Ser Gly Gly Thr Ser Ser Asn Gly Leu Tyr Pro Arg Lys Lys Thr Val Leu Asn Met
AGC GGC GGT ACG TCC TCC AAC GGT CTG TAC CCG CGT AAG AAG ACT GTT CTC AAC ATG
      1713        1722        1731        1740        1749        1758

Val Asn Val Asn Phe Tyr Gly Pro Gly Met Thr Glu Gly Ala Leu Tyr Ser Lys Ala
GTG AAC GTG AAC TTC TAC GGG CCG GGC ATG ACC GAG GGT GCG CTG TAC AGT AAG GCT
      1770        1779        1788        1797        1806        1815
```

FIG. 1C

```
Arg Tyr Ser Asp Ile Ser Thr Leu Asn Ser Asn Val Arg Ala Ile Pro Tyr Thr Asn
CGC TAC TCG GAT ATC AGC ACG CTG AAC TCC AAC GTG CGT GCT ATC CCG TAC ACC AAC
      1827       1836       1845       1854       1863       1872

Ile Gln Gly Asn Val Gly Val Ile Leu Ser Pro Val Asn Arg Met Tyr Thr Leu Pro
ATC CAA GGT AAC GTG GGT GTC ATC CTG TCT CCG GTC AAC CGC ATG TAC ACG CTG CCG
      1884       1893       1902       1911       1920       1929

Asn Ala Leu Ala Thr Leu Asp Gly Asn Glu Phe Pro Thr Gly Lys Glu Phe Cys Glu
AAC GCC CTC GCT ACC CTT GAC GGT AAT GAG TTC CCC ACC GGG AAA GAG TTC TGC GAA
      1941       1950       1959       1968       1977       1986

Gly Thr Val Leu Phe Lys Thr Asp Gly Ser Gly Gly Asn Phe Ile Val Thr Arg Phe
GGT ACT GTG CTG TTC AAG ACC GAT GGC TCC GGT GGC AAC TTC ATC GTG ACC CGG TTC
      1998       2007       2016       2025       2034       2043

Gly Ala Tyr Ile Pro Asp Asp Gly Asn Asn Phe Lys Val Arg Ala Ala Ala Ala Gly
GGT GCG TAC ATC CCG GAT GAC GGT AAC AAC TTC AAG GTG CGT GCT GCT GCC GCT GGC
      2055       2064       2073       2082       2091       2100

Gln Thr Tyr Leu Glu Gln Asn Leu Thr Pro Ala Gly Thr Gln Ala Ser Thr Ser Trp
CAG ACG TAT CTG GAG CAG AAC CTG ACT CCG GCT GGT ACT CAG GCT TCC ACC TCG TGG
      2112       2121       2130       2139       2148       2157

Leu Tyr His Lys Pro Ile Ser Ala Gly Thr Arg Leu Asn Val Pro Gly Ala Gly Pro
CTG TAC CAT AAG CCA ATC TCT GCT GGT ACT CGA CTC AAT GTT CCG GGT GCC GGG CCG
      2169       2178       2187       2196       2205       2214

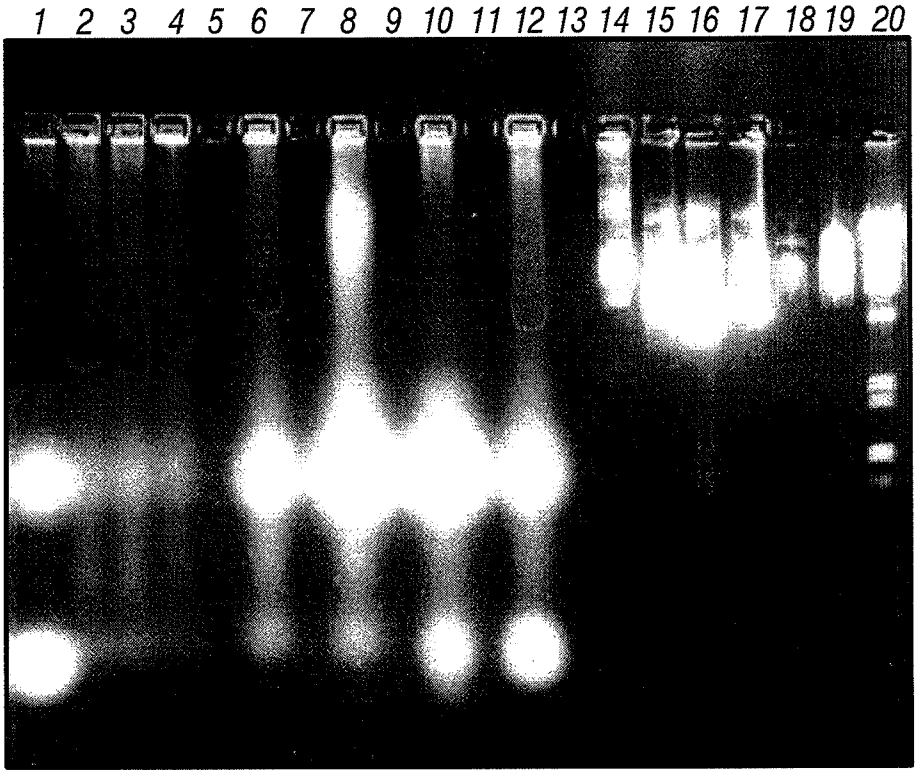
Ser Gly Gly Thr Leu Thr Val Thr Val Val Arg Ala Pro Tyr Gln Val Asp Asn Asn
AGC GGC GGT ACG CTC ACT GTG ACG GTG GTG CGT GCT CCG TAT CAG GTG GAC AAC AAC
      2226       2235       2244       2253       2262       2271

Ile Gly Asn Pro Val Arg Ile Asp Ile Thr Pro Ala Ile Val Thr Ala Ile Pro Ala
ATC GGA AAC CCG GTA CGC ATC GAC ATT ACC CCG GCC ATT GTG ACG GCA ATC CCT GCG
      2283       2292       2301       2310       2319       2328

Gly Thr Gln Leu Ala Ala Thr Tyr Pro Val Ala Try Ile TER
GGA ACG CAG CTC GCC GCT ACC TAC CCG GTG GCT TAC ATC TAA
      2340       2349       2358       2367
```

FIG. 1D

Fig. 2



Lane#	Sample
1	Laboratory Grade plasmid DNA, Prep A labeled with DTAF
2	GMP Grade DNA, Company #2 labeled with DTAF
3	GMP Grade DNA, Company #1 labeled with DTAF
4	Clinical Grade DNA, Company #1 labeled with DTAF
5	No Sample Loaded
6	Qiagen Endotoxin free DNA, Prep A Labeled with DTAF
7	No Sample Loaded
8	Detoxified LPS, Sigma, labeled with DTAF
9	No Sample Loaded
10	LPS, Sigma, labeled with DTAF
11	No Sample Loaded
12	Laboratory Grade plasmid DNA, Prep B labeled with DTAF
13	No Sample Loaded
14	Laboratory Grade plasmid DNA, Prep A labeled with EtBr
15	GMP Grade DNA, Company #2 labeled with EtBr
16	GMP Grade DNA, Company #1 labeled with EtBr
17	Clinical Grade DNA, Company #1 labeled with EtBr
18	Laboratory Grade plasmid DNA, Prep B labeled with EtBr
19	Qiagen Endotoxin free DNA, Prep A Labeled with EtBr
20	Mixture of high and low DNA molecular weight markers labeled with EtBr

Fig. 3

SEQ ID NO: 1 - - CAE Full-length Protein Sequence

MANSYNAYVANGSQTAFLVTFEQRVFTEIQVYLNSELQTEGYTYNSVTKQIIFDTAPLAGVIVRLQRYTSEVLLNKFGQDAAFTGQNLDE
NFEQILFKAEETQEAWLAPLDRAVRVPNSEVSINALPNVAGRRNKALGFDSNGQPFMIPLVDIPDSALAIALAMADGGKWIGTLGGGTFL
DRQDTVCLSEFTNNTGYASVAAAVQACFDYAKANGKVVDARGWEGTVDSTVLMDGIEVVGGTWHGKADIRLLNSTFRNFVASTVRVA
YWGGEVRIADYEFTSAPSNSKVTSILFQGNIAGGSYVIENGIHRNGKFGILQQGTGEAITNGVIRGITMMDMQGDGIEMNVINKHYDGGL
LIENIFLENIDGTNAPIPLSNWGIGIGIAGQGPFGWDAAETQYAKNVTVRNVHAPRGVRQVVHFEVTRDSTCENVVANPDLSVSIGTGLT
AAGVITYGCKRMTIDGVVGEPMNTGATSPNDIRIVMLEWGANQAGAGGTPGAACPSFDMTVRNVQTRTGRFYAGVGSDDDNTNTYH
LENIHCYKMTLFGVATLLNMTNVTGVVFDAVGDDSSGGTSSNGLYPRKKTVLNMVNVNFYGPGMTEGALYSKARYSDISTLNSNVRAI
PYTNIQGNVGVILSPVNRMYTLPNALATLDGNEFPTGKEFCEGTVLFKTDGSGGNFIVTRFGAYIPDDGNNFKVRAAAAGQTYLEQNLT
PAGTQASTSWLYHKPISAGTRLNVPGAGPSGGTLTVTVVRAPYQVDNNIGNPVRIDITPAIVTAIPAGTQLAATYPVAYI

Fig. 4

SEQ ID NO: 2 - - CAE Truncated Protein Sequence

LAPLDRAVRVPNSEVSINALPNVAGRRNKALGFDSNGQPFMIPLVDIPDSALAIALAMADGGKWIGTLGGGTFLDRQDTVCLSEFTNNT
GYASVAAAVQACFDYAKANGKVVDARGWEGTVDSTVLMDGIEVVGGTWHGKADIRLLNSTFRNFVASTVRVAYWGGEVRIADYEFTS
APSNSKVTSILFQGNIAGGSYVIENGIHRNGKFGILQQGTGEAITNGVIRGITMMDMQGDGIEMNVINKHYDGGLLIENIFLENIDGTNAPI
PLSNWGIGIGIAGQGPFGWDAAETQYAKNVTVRNVHAPRGVRQVVHFEVTRDSTCENVVANPDLSVSIGTGLTAAGVITYGCKRMTID
GVVGEPMNTGATSPNDIRIVMLEWGANQAGAGGTPGAACPSFDMTVRNVQTRTGRFYAGVGSDDDNTNTYHLENIHCYKMTLFGVA
TLLNMTNVTGVVFDAVGDDSSGGTSSNGLYPRKKTVLNMVNVNFYGPGMTEGALYSKARYSDISTLNSNVRAIPYTNIQGNVGVILSPV
NRMYTLPNALATLDGNEFPTGKEFCEGTVLFKTDGSGGNFIVTRFGAYIPDDGNNFKVRAAAAGQTYLEQNLTPAGTQASTSWLYHKP
ISAGTRLNVPGAGPSGGTLTVTVVRAPYQVDNNIGNPVRIDITPAIVTAIPAGTQLAATYPVAYI

Fig. 5

SEQ ID NO: 3 - - HIS-Tagged CAE Full-length Protein Sequence

MGHHHHHHMANSYNAYVANGSQTAFLVTFEQRVFTEIQVYLNSELQTEGYTYNSVTKQIIFDTAPLAGVIVRLQRYTSEVLLNKFGQDA
AFTGQNLDENFEQILFKAEETQEAWLAPLDRAVRVPNSEVSINALPNVAGRRNKALGFDSNGQPFMIPLVDIPDSALAIALAMADGGKWI
GTLGGGTFLDRQDTVCLSEFTNNTGYASVAAAVQACFDYAKANGKVVDARGWEGTVDSTVLMDGIEVVGGTWHGKADIRLLNSTFRN
FVASTVRVAYWGGEVRIADYEFTSAPSNSKVTSILFQGNIAGGSYVIENGIHRNGKFGILQQGTGEAITNGVIRGITMMDMQGDGIEMNV
INKHYDGGLLIENIFLENIDGTNAPIPLSNWGIGIGIAGQGPFGWDAAETQYAKNVTVRNVHAPRGVRQVVHFEVTRDSTCENVVANPDL
SVSIGTGLTAAGVITYGCKRMTIDGVVGEPMNTGATSPNDIRIVMLEWGANQAGAGGTPGAACPSFDMTVRNVQTRTGRFYAGVGSD
DDNTNTYHLENIHCYKMTLFGVATLLNMTNVTGVVFDAVGDDSSGGTSSNGLYPRKKTVLNMVNVNFYGPGMTEGALYSKARYSDIST
LNSNVRAIPYTNIQGNVGVILSPVNRMYTLPNALATLDGNEFPTGKEFCEGTVLFKTDGSGGNFIVTRFGAYIPDDGNNFKVRAAAAGQ
TYLEQNLTPAGTQASTSWLYHKPISAGTRLNVPGAGPSGGTLTVTVVRAPYQVDNNIGNPVRIDITPAIVTAIPAGTQLAATYPVAYI

Fig. 6

SEQ ID NO: 4 - - HIS-Tagged CAE Truncated Protein Sequence

MGHHHHHHLAPLDRAVRVPNSEVSINALPNVAGRRNKALGFDSNGQPFMIPLVDIPDSALAIALAMADGGKWIGTLGGGTFLDRQDTV
CLSEFTNNTGYASVAAAVQACFDYAKANGKVVDARGWEGTVDSTVLMDGIEVVGGTWHGKADIRLLNSTFRNFVASTVRVAYWGGE
VRIADYEFTSAPSNSKVTSILFQGNIAGGSYVIENGIHRNGKFGILQQGTGEAITNGVIRGITMMDMQGDGIEMNVINKHYDGGLLIENIFL
ENIDGTNAPIPLSNWGIGIGIAGQGPFGWDAAETQYAKNVTVRNVHAPRGVRQVVHFEVTRDSTCENVVANPDLSVSIGTGLTAAGVIT
YGCKRMTIDGVVGEPMNTGATSPNDIRIVMLEWGANQAGAGGTPGAACPSFDMTVRNVQTRTGRFYAGVGSDDDNTNTYHLENIHC
YKMTLFGVATLLNMTNVTGVVFDAVGDDSSGGTSSNGLYPRKKTVLNMVNVNFYGPGMTEGALYSKARYSDISTLNSNVRAIPYTNIQ
GNVGVILSPVNRMYTLPNALATLDGNEFPTGKEFCEGTVLFKTDGSGGNFIVTRFGAYIPDDGNNFKVRAAAAGQTYLEQNLTPAGTQ
ASTSWLYHKPISAGTRLNVPGAGPSGGTLTVTVVRAPYQVDNNIGNPVRIDITPAIVTAIPAGTQLAATYPVAYI

Fig. 7

SEQ ID NO: 5 - - FLAG®-Tagged CAE Full-length Protein Sequence

MANSYNAYVANGSQTAFLVTFEQRVFTEIQVYLNSELQTEGYTYNSVTKQIIFDTAPLAGVIVRLQRYTSEVLLNKFGQDAAFTGQNLDE
NFEQILFKAEETQEAWLAPLDRAVRVPNSEVSINALPNVAGRRNKALGFDSNGQPFMIPLVDIPDSALAIALAMADGGKWIGTLGGGTFL
DRQDTVCLSEFTNNTGYASVAAAVQACFDYAKANGKVVDARGWEGTVDSTVLMDGIEVVGGTWHGKADIRLLNSTFRNFVASTVRVA
YWGGEVRIADYEFTSAPSNSKVTSILFQGNIAGGSYVIENGIHRNGKFGILQQGTGEAITNGVIRGITMMDMQGDGIEMNVINKHYDGGL
LIENIFLENIDGTNAPIPLSNWGIGIGIAGQGGPFGWDAAETQYAKNVTVRNVHAPRGVRQVVHFEVTRDSTCENVVANPDLSVSIGTGLT
AAGVITYGCKRMTIDGVVGEPMNTGATSPNDIRIVMLEWGANQAGAGGTPGAACPSFDMTVRNVQTRTGRFYAGVGSDDDNTNTYH
LENIHCYKMTLFGVATLLNMTNVTGVVFDAVGDDSSGGTSSNGLYPRKKTVLNMVNVNFYGPGMTEGALYSKARYSDISTLNSNVRAI
PYTNIQGNVGVILSPVNRMYTLPNALATLDGNEFPTGKEFCEGTVLFKTDGSGGNFIVTRFGAYIPDDGNNFKVRAAAAGQTYLEQNLT
PAGTQASTSWLYHKPISAGTRLNVPGAGPSGGTLTVTVVRAPYQVDNNIGNPVRIDITPAIVTAIPAGTQLAATYPVAYIDYKDDDDK

Fig. 8

SEQ ID NO: 6 - - FLAG®-Tagged CAE Truncated Protein Sequence

LAPLDRAVRVPNSEVSINALPNVAGRRNKALGFDSNGQPFMIPLVDIPDSALAIALAMADGGKWIGTLGGGTFLDRQDTVCLSEFTNNT
GYASVAAAVQACFDYAKANGKVVDARGWEGTVDSTVLMDGIEVVGGTWHGKADIRLLNSTFRNFVASTVRVAYWGGEVRIADYEFTS
APSNSKVTSILFQGNIAGGSYVIENGIHRNGKFGILQQGTGEAITNGVIRGITMMDMQGDGIEMNVINKHYDGGLLIENIFLENIDGTNAPI
PLSNWGIGIGIAGQGPFGWDAAETQYAKNVTVRNVHAPRGVRQVVHFEVTRDSTCENVVANPDLSVSIGTGLTAAGVITYGCKRMTID
GVVGEPMNTGATSPNDIRIVMLEWGANQAGAGGTPGAACPSFDMTVRNVQTRTGRFYAGVGSDDDNTNTYHLENIHCYKMTLFGVA
TLLNMTNVTGVVFDAVGDDSSGGTSSNGLYPRKKTVLNMVNVNFYGPGMTEGALYSKARYSDISTLNSNVRAIPYTNIQGNVGVILSPV
NRMYTLPNALATLDGNEFPTGKEFCEGTVLFKTDGSGGNFIVTRFGAYIPDDGNNFKVRAAAAGQTYLEQNLTPAGTQASTSWLYHKP
ISAGTRLNVPGAGPSGGTLTVTVVRAPYQVDNNIGNPVRIDITPAIVTAIPAGTQLAATYPVAYIDYKDDDDK

Fig. 9

SEQ ID NO: 7 - - CAE Full-Length DNA Coding Sequence

ATGGCGAACA GCTATAATGC TTACGTGGCG AACGGTTCAC AGACCGCATT CCTCGTCACG TTCGAGCAGC GCGTGTTCAC
TGAGATTCAG GTGTACCTCA ACTCCGAACT CCAGACGGAA GGGTACACCT ACAACTCTGT GACCAAACAG ATTATCTTCG
ACACCGCCCC GCTCGCCGGG GTGATTGTCC GACTCCAACG CTACACCTCT GAGGTTCTGC TGAACAAGTT GGCCAAGAC
GCTGCCTTCA CCGGGCAGAA CCTTGACGAG AACTTTGAGC AGATTCTGTT CAAGGCTGAG GAAACTCAGG AAGCATGGCT
CGCGCCACTT GACCGCGCCG TCCGTGTTCC GAACTCCGAA GTCTCCATCA ACGCATTACC GAACGTCGCT GCCGCCGCA
ACAAGGCACT GGGCTTTGAC AGCAATGGTC AGCCGTTCAT GATTCCTCTG GTCGATATCC CGGACTCCGC GCTGGCGATT
GCTCTGGCAA TGGCTGACGG CGGTAAGTGG ATTGGTACTC TCGGCGGGGG CACGTTCCTC GACCGTCAGG ATACCGTCTG
CCTGTCCGAG TTCACCAACA ACACTGGGTA CGCCTCTGTC GCCGCTGCGG TGCAGGCTTG CTTCGACTAT GCGAAAGCCA
ACGGCAAGGT CGTTGACGCT CGCGGCTGGG AAGGTACGGT GGATTCCACT GTGCTGATGG ACGGTATTGA GGTCGTCGGC
GGTACGTGGC ACGGCAAGGC TGACATTCGC CTGCTGAACT CCACCTTCCG CAACTTCGTG GCCTCTACTG TCCGTGTCGC
CTACTGGGGC GGCGAGGTGC GTATTGCTGA CTATGAGTTC ACCAGCGCAC CGAGCAACTC CAAGGTTACG TCTATCCTGT
TCCAAGGCAA CATCGCCGGG GGCAGCTACG TCATTGAGAA CGGTATCCAC CGCAATGGTA AGTTCGGTAT TCTCCAACAG
GGTACTGGCG AGGCTATCAC CAACGGCGTT ATCCGTGGCA TCACCATGAT GGATATGCAG GGTGACGGTA TCGAGATGAA
CGTAATCAAC AAGCACTATG ATGGTGGCCT GCTGATTGAG AACATCTTCC TTGAGAACAT CGACGGCACC AACGCGCCTA
TCCCACTGTC CAACTGGGGC ATTGGTATCG GTATCGCTGG TCAAGGCCCG TTCGGTTGGG ATGCTGCTGA GACGCAGTAT
GCGAAGAACG TCACTGTCCG TAACGTCCAT GCTCCGCGTG GTGTGCGTCA GGTCGTCCAC TTCGAGGTTA CGCGTGACAG
CACCTGCGAG AACGTAGTGG CCAACCCTGA CCTGTCCGTC TCCATTGGTA CTGGCCTGAC TGCCGCTGGT GTAATCACGT
ACGGCTGCAA GCGCATGACC ATTGACGGTG TAGTCGGTGA GCCTATGAAC ACCGGAGCAA CCTCTCCGAA CGATATTCGT
ATCGTGATGT TGGAGTGGGG TGCGAACCAA GCAGGTGCTG GCGGTACGCC GGGTGCAGCT TGCCCATCGT TCGACATGAC
CGTGCGTAAC GTGCAGACCC GTACCGGGCG CTTCTATGCT GGTGTCGGCT CCGACGATGA CAACACCAAC ACATATCACC
TTGAAAACAT TCACTGTTAC AAGATGACGC TGTTTGGTGT GGCAACTCTG CTGAACATGA CCAACGTGAC TGGTGTGGTG
TTCGACGCTG TAGGCGATGA CTCCAGCGGC GGTACGTCCT CCAACGGTCT GTACCCGCGT AAGAAGACTG TTCTCAACAT
GGTGAACGTG AACTTCTACG GGCCGGGCAT GACCGAGGGT GCGCTGTACA GTAAGGCTCG CTACTCGGAT ATCAGCACGC
TGAACTCCAA CGTGCGTGCT ATCCCGTACA CCAACATCCA AGGTAACGTG GGTGTCATCC TGTCTCCGGT CAACCGCATG
TACACGCTGC CGAACGCCCT CGCTACCCTT GACGGTAATG AGTTCCCCAC CGGGAAAGAG TTCTGCGAAG GTACTGTGCT
GTTCAAGACC GATGGCTCCG GTGGCAACTT CATCGTGACC CGGTTCGGTG CGTACATCCC GGATGACGGT AACAACTTCA
AGGTGCGTGC TGCTGCCGCT GGCCAGACGT ATCTGGAGCA GAACCTGACT CCGGCTGGTA CTCAGGCTTC CACCTCGTGG
CTGTACCATA AGCCAATCTC TGCTGGTACT CGACTCAATG TTCCGGGTGC CGGGCCGAGC GGCGGTACGC TCACTGTGAC
GGTGGTGCGT GCTCCGTATC AGGTGGACAA CAACATCGGA AACCCGGTAC GCATCGACAT TACCCCGGCC ATTGTGACGG
CAATCCCTGC GGGAACGCAG CTCGCCGCTA CCTACCCGGT GGCTTACATC TAA

Fig. 10

SEQ ID NO: 8 - - CAE Truncated DNA Coding Sequence

CTCGCGCCAC TTGACCGCGC CGTCCGTGTT CCGAACTCCG AAGTCTCCAT CAACGCATTA CCGAACGTCG CTGGCCGCCG
CAACAAGGCA CTGGGCTTTG ACAGCAATGG TCAGCCGTTC ATGATTCCTC TGGTCGATAT CCCGGACTCC GCGCTGGCGA
TTGCTCTGGC AATGGCTGAC GGCGGTAAGT GGATTGGTAC TCTCGGCGGG GGCACGTTCC TCGACCGTCA GGATACCGTC
TGCCTGTCCG AGTTCACCAA CAACACTGGG TACGCCTCTG TCGCCGCTGC GGTGCAGGCT TGCTTCGACT ATGCGAAAGC
CAACGGCAAG GTCGTTGACG CTCGCGGCTG GGAAGGTACG GTGGATTCCA CTGTGCTGAT GGACGGTATT GAGGTCGTCG
GCGGTACGTG GCACGGCAAG GCTGACATTC GCCTGCTGAA CTCCACCTTC CGCAACTTCG TGGCCTCTAC TGTCCGTGTC
GCCTACTGGG GCGGCGAGGT GCGTATTGCT GACTATGAGT TCACCAGCGC ACCGAGCAAC TCCAAGGTTA CGTCTATCCT
GTTCCAAGGC AACATCGCCG GGGGCAGCTA CGTCATTGAG AACGGTATCC ACCGCAATGG TAAGTTCGGT ATTCTCCAAC
AGGGTACTGG CGAGGCTATC ACCAACGGCG TTATCCGTGG CATCACCATG ATGGATATGC AGGGTGACGG TATCGAGATG
AACGTAATCA ACAAGCACTA TGATGGTGGC CTGCTGATTG AGAACATCTT CCTTGAGAAC ATCGACGGCA CCAACGCGCC
TATCCCACTG TCCAACTGGG GCATTGGTAT CGGTATCGCT GGTCAAGGCC CGTTCGGTTG GGATGCTGCT GAGACGCAGT
ATGCGAAGAA CGTCACTGTC CGTAACGTCC ATGCTCCGCG TGGTGTGCGT CAGGTCGTCC ACTTCGAGGT TACGCGTGAC
AGCACCTGCG AGAACGTAGT GGCCAACCCT GACCTGTCCG TCTCCATTGG TACTGGCCTG ACTGCCGCTG GTGTAATCAC
GTACGGCTGC AAGCGCATGA CCATTGACGG TGTAGTCGGT GAGCCTATGA ACACCGGAGC AACCTCTCCG AACGATATTC
GTATCGTGAT GTTGGAGTGG GGTGCGAACC AAGCAGGTGC TGGCGGTACG CCGGGTGCAG CTTGCCCATC GTTCGACATG
ACCGTGCGTA ACGTGCAGAC CCGTACCGGG CGCTTCTATG CTGGTGTCGG CTCCGACGAT GACAACACCA ACACATATCA
CCTTGAAAAC ATTCACTGTT ACAAGATGAC GCTGTTTGGT GTGGCAACTC TGCTGAACAT GACCAACGTG ACTGGTGTGG
TGTTCGACGC TGTAGGCGAT GACTCCAGCG GCGGTACGTC CTCCAACGGT CTGTACCCGC GTAAGAAGAC TGTTCTCAAC
ATGGTGAACG TGAACTTCTA CGGGCCGGGC ATGACCGAGG GTGCGCTGTA CAGTAAGGCT CGCTACTCGG ATATCAGCAC
GCTGAACTCC AACGTGCGTG CTATCCCGTA CACCAACATC CAAGGTAACG TGGGTGTCAT CCTGTCTCCG GTCAACCGCA
TGTACACGCT GCCGAACGCC CTCGCTACCC TTGACGGTAA TGAGTTCCCC ACCGGGAAAG AGTTCTGCGA AGGTACTGTG
CTGTTCAAGA CCGATGGCTC CGGTGGCAAC TTCATCGTGA CCCGGTTCGG TGCGTACATC CCGGATGACG GTAACAACTT
CAAGGTGCGT GCTGCTGCCG CTGGCCAGAC GTATCTGGAG CAGAACCTGA CTCCGGCTGG TACTCAGGCT TCCACCTCGT
GGCTGTACCA TAAGCCAATC TCTGCTGGTA CTCGACTCAA TGTTCCGGGT GCCGGGCCGA GCGGCGGTAC GCTCACTGTG
ACGGTGGTGC GTGCTCCGTA TCAGGTGGAC AACAACATCG GAAACCCGGT ACGCATCGAC ATTACCCCGG CCATTGTGAC
GGCAATCCCT GCGGGAACGC AGCTCGCCGC TACCTACCCG GTGGCTTACA TCTAA

Fig. 11

SEQ ID NO: 9 - - CAE Fragment

ANSYNAYVANGSQTA

SEQ ID NO: 10 - - CAE Fragment

LLEQGTGEALTDGVLR

SEQ ID NO: 11 - - CAE Fragment

VPNSEVSLNALPNVQR

SEQ ID NO: 12 - - CAE Fragment

LADYEFTSAPSNSK

SEQ ID NO: 13 - - CAE Fragment

YSDLSTLN

SEQ ID NO: 14 - - CAE Fragment

QLLFDTAPLA

SEQ ID NO: 15 - - CAE Fragment

APYQVDDNL

SEQ ID NO: 16 - - CAE Fragment

FGAYLPDD

SEQ ID NO: 17 - - CAE Fragment

LGTLGG

Fig. 12

TOXICITY MEASUREMENTS *

DNA Type	DNA Amount	# of Mice Injected	# of Dead Mice at 18 hours Post-Injection	# of Dead Mice at 1 Week Post-Injection
Super Clean	100 µg	10	0	0
Super Clean	50 µg	10	0	0
Qiagen EndoFree	100 µg	10	10	N/A
Qiagen EndoFree	50 µg	10	0	0

* Experiments performed in Balb/c mice using PDX-1 shRNA Super Clean DNA versus PDX-1 shRNA Qiagen EndoFree DNA

Fig. 13

TOXICITY MEASUREMENTS *

DNA Type	DNA Amount	# of Mice Injected	# of Dead Mice at 18 hours Post-Injection	# of Dead Mice at 3 Weeks Post-Injection
Super Clean	100 µg	20	0	0
Super Clean	40 µg	20	0	0
Qiagen EndoFree	100 µg	5	5	N/A
Qiagen EndoFree	40 µg	5	5	N/A

* Experiments performed in SCID mice using the CAE enzyme method for Super Clean DNA production

Fig. 14

TOXICITY MEASUREMENTS *

DNA Type	DNA Amount	# of Mice Injected	# of Dead Mice at 18 hours Post-Injection	# of Dead Mice at 3 Weeks Post-Injection
Super Clean	100 µg	60	0	0
Qiagen EndoFree	100 µg	5	5	N/A

* Experiments performed in PANC-1 tumor-bearing SCID mice using the CAE enzyme method for Super Clean DNA production

SequenceListing

SEQUENCE LISTING

<110> Gradalis, Inc.

<120> Highly Pure Plasmid DNA Preparations and Processes for Preparing the Same

<130> Gradalis, Inc.

<150> 61/125,916
<151> 2008-04-30

<150> 61/125,923
<151> 2008-04-30

<160> 17

<170> PatentIn version 3.4

<210> 1
<211> 790
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence for colanic acid degrading enzyme (CAE), derived from Bacteriophage (NST1).

<400> 1

Met Ala Asn Ser Tyr Asn Ala Tyr Val Ala Asn Gly Ser Gln Thr Ala
1 5 10 15

Phe Leu Val Thr Phe Glu Gln Arg Val Phe Thr Glu Ile Gln Val Tyr
20 25 30

Leu Asn Ser Glu Leu Gln Thr Glu Gly Tyr Thr Tyr Asn Ser Val Thr
35 40 45

Lys Gln Ile Ile Phe Asp Thr Ala Pro Leu Ala Gly Val Ile Val Arg
50 55 60

Leu Gln Arg Tyr Thr Ser Glu Val Leu Leu Asn Lys Phe Gly Gln Asp
65 70 75 80

Ala Ala Phe Thr Gly Gln Asn Leu Asp Glu Asn Phe Glu Gln Ile Leu
85 90 95

Phe Lys Ala Glu Glu Thr Gln Glu Ala Trp Leu Ala Pro Leu Asp Arg
100 105 110

Ala Val Arg Val Pro Asn Ser Glu Val Ser Ile Asn Ala Leu Pro Asn
115 120 125

Val Ala Gly Arg Arg Asn Lys Ala Leu Gly Phe Asp Ser Asn Gly Gln
130 135 140

Pro Phe Met Ile Pro Leu Val Asp Ile Pro Asp Ser Ala Leu Ala Ile
145 150 155 160

SequenceListing

```
Ala Leu Ala Met Ala Asp Gly Gly Lys Trp Ile Gly Thr Leu Gly Gly
                165                 170                 175

Gly Thr Phe Leu Asp Arg Gln Asp Thr Val Cys Leu Ser Glu Phe Thr
            180                 185                 190

Asn Asn Thr Gly Tyr Ala Ser Val Ala Ala Ala Val Gln Ala Cys Phe
        195                 200                 205

Asp Tyr Ala Lys Ala Asn Gly Lys Val Val Asp Ala Arg Gly Trp Glu
    210                 215                 220

Gly Thr Val Asp Ser Thr Val Leu Met Asp Gly Ile Glu Val Val Gly
225                 230                 235                 240

Gly Thr Trp His Gly Lys Ala Asp Ile Arg Leu Leu Asn Ser Thr Phe
                245                 250                 255

Arg Asn Phe Val Ala Ser Thr Val Arg Val Ala Tyr Trp Gly Gly Glu
            260                 265                 270

Val Arg Ile Ala Asp Tyr Glu Phe Thr Ser Ala Pro Ser Asn Ser Lys
        275                 280                 285

Val Thr Ser Ile Leu Phe Gln Gly Asn Ile Ala Gly Gly Ser Tyr Val
    290                 295                 300

Ile Glu Asn Gly Ile His Arg Asn Gly Lys Phe Gly Ile Leu Gln Gln
305                 310                 315                 320

Gly Thr Gly Glu Ala Ile Thr Asn Gly Val Ile Arg Gly Ile Thr Met
                325                 330                 335

Met Asp Met Gln Gly Asp Gly Ile Glu Met Asn Val Ile Asn Lys His
            340                 345                 350

Tyr Asp Gly Gly Leu Leu Ile Glu Asn Ile Phe Leu Glu Asn Ile Asp
        355                 360                 365

Gly Thr Asn Ala Pro Ile Pro Leu Ser Asn Trp Gly Ile Gly Ile Gly
    370                 375                 380

Ile Ala Gly Gln Gly Pro Phe Gly Trp Asp Ala Ala Glu Thr Gln Tyr
385                 390                 395                 400

Ala Lys Asn Val Thr Val Arg Asn Val His Ala Pro Arg Gly Val Arg
                405                 410                 415

Gln Val Val His Phe Glu Val Thr Arg Asp Ser Thr Cys Glu Asn Val
            420                 425                 430
```

SequenceListing

```
Val Ala Asn Pro Asp Leu Ser Val Ser Ile Gly Thr Gly Leu Thr Ala
        435                 440                 445

Ala Gly Val Ile Thr Tyr Gly Cys Lys Arg Met Thr Ile Asp Gly Val
    450                 455                 460

Val Gly Glu Pro Met Asn Thr Gly Ala Thr Ser Pro Asn Asp Ile Arg
465                 470                 475                 480

Ile Val Met Leu Glu Trp Gly Ala Asn Gln Ala Gly Ala Gly Gly Thr
                485                 490                 495

Pro Gly Ala Ala Cys Pro Ser Phe Asp Met Thr Val Arg Asn Val Gln
            500                 505                 510

Thr Arg Thr Gly Arg Phe Tyr Ala Gly Val Gly Ser Asp Asp Asp Asn
        515                 520                 525

Thr Asn Thr Tyr His Leu Glu Asn Ile His Cys Tyr Lys Met Thr Leu
    530                 535                 540

Phe Gly Val Ala Thr Leu Leu Asn Met Thr Asn Val Thr Gly Val Val
545                 550                 555                 560

Phe Asp Ala Val Gly Asp Asp Ser Ser Gly Gly Thr Ser Ser Asn Gly
                565                 570                 575

Leu Tyr Pro Arg Lys Lys Thr Val Leu Asn Met Val Asn Val Asn Phe
            580                 585                 590

Tyr Gly Pro Gly Met Thr Glu Gly Ala Leu Tyr Ser Lys Ala Arg Tyr
        595                 600                 605

Ser Asp Ile Ser Thr Leu Asn Ser Asn Val Arg Ala Ile Pro Tyr Thr
    610                 615                 620

Asn Ile Gln Gly Asn Val Gly Val Ile Leu Ser Pro Val Asn Arg Met
625                 630                 635                 640

Tyr Thr Leu Pro Asn Ala Leu Ala Thr Leu Asp Gly Asn Glu Phe Pro
                645                 650                 655

Thr Gly Lys Glu Phe Cys Glu Gly Thr Val Leu Phe Lys Thr Asp Gly
            660                 665                 670

Ser Gly Gly Asn Phe Ile Val Thr Arg Phe Gly Ala Tyr Ile Pro Asp
        675                 680                 685

Asp Gly Asn Asn Phe Lys Val Arg Ala Ala Ala Ala Gly Gln Thr Tyr
    690                 695                 700
```

SequenceListing

```
Leu Glu Gln Asn Leu Thr Pro Ala Gly Thr Gln Ala Ser Thr Ser Trp
705                 710                 715                 720

Leu Tyr His Lys Pro Ile Ser Ala Gly Thr Arg Leu Asn Val Pro Gly
                725                 730                 735

Ala Gly Pro Ser Gly Gly Thr Leu Thr Val Thr Val Val Arg Ala Pro
            740                 745                 750

Tyr Gln Val Asp Asn Asn Ile Gly Asn Pro Val Arg Ile Asp Ile Thr
        755                 760                 765

Pro Ala Ile Val Thr Ala Ile Pro Ala Gly Thr Gln Leu Ala Ala Thr
    770                 775                 780

Tyr Pro Val Ala Tyr Ile
785                 790
```

<210> 2
<211> 684
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence for truncated colanic acid degrading enzyme (CAE).

<400> 2

```
Leu Ala Pro Leu Asp Arg Ala Val Arg Val Pro Asn Ser Glu Val Ser
1               5                   10                  15

Ile Asn Ala Leu Pro Asn Val Ala Gly Arg Arg Asn Lys Ala Leu Gly
            20                  25                  30

Phe Asp Ser Asn Gly Gln Pro Phe Met Ile Pro Leu Val Asp Ile Pro
        35                  40                  45

Asp Ser Ala Leu Ala Ile Ala Leu Ala Met Ala Asp Gly Gly Lys Trp
    50                  55                  60

Ile Gly Thr Leu Gly Gly Gly Thr Phe Leu Asp Arg Gln Asp Thr Val
65                  70                  75                  80

Cys Leu Ser Glu Phe Thr Asn Asn Thr Gly Tyr Ala Ser Val Ala Ala
                85                  90                  95

Ala Val Gln Ala Cys Phe Asp Tyr Ala Lys Ala Asn Gly Lys Val Val
            100                 105                 110

Asp Ala Arg Gly Trp Glu Gly Thr Val Asp Ser Thr Val Leu Met Asp
        115                 120                 125
```

SequenceListing

```
Gly Ile Glu Val Val Gly Gly Thr Trp His Gly Lys Ala Asp Ile Arg
    130                 135                 140

Leu Leu Asn Ser Thr Phe Arg Asn Phe Val Ala Ser Thr Val Arg Val
145                 150                 155                 160

Ala Tyr Trp Gly Gly Glu Val Arg Ile Ala Asp Tyr Glu Phe Thr Ser
                165                 170                 175

Ala Pro Ser Asn Ser Lys Val Thr Ser Ile Leu Phe Gln Gly Asn Ile
            180                 185                 190

Ala Gly Gly Ser Tyr Val Ile Glu Asn Gly Ile His Arg Asn Gly Lys
        195                 200                 205

Phe Gly Ile Leu Gln Gln Gly Thr Gly Glu Ala Ile Thr Asn Gly Val
    210                 215                 220

Ile Arg Gly Ile Thr Met Met Asp Met Gln Gly Asp Gly Ile Glu Met
225                 230                 235                 240

Asn Val Ile Asn Lys His Tyr Asp Gly Gly Leu Leu Ile Glu Asn Ile
                245                 250                 255

Phe Leu Glu Asn Ile Asp Gly Thr Asn Ala Pro Ile Pro Leu Ser Asn
            260                 265                 270

Trp Gly Ile Gly Ile Gly Ile Ala Gly Gln Gly Pro Phe Gly Trp Asp
        275                 280                 285

Ala Ala Glu Thr Gln Tyr Ala Lys Asn Val Thr Val Arg Asn Val His
    290                 295                 300

Ala Pro Arg Gly Val Arg Gln Val Val His Phe Glu Val Thr Arg Asp
305                 310                 315                 320

Ser Thr Cys Glu Asn Val Val Ala Asn Pro Asp Leu Ser Val Ser Ile
                325                 330                 335

Gly Thr Gly Leu Thr Ala Ala Gly Val Ile Thr Tyr Gly Cys Lys Arg
            340                 345                 350

Met Thr Ile Asp Gly Val Val Gly Glu Pro Met Asn Thr Gly Ala Thr
        355                 360                 365

Ser Pro Asn Asp Ile Arg Ile Val Met Leu Glu Trp Gly Ala Asn Gln
    370                 375                 380

Ala Gly Ala Gly Gly Thr Pro Gly Ala Ala Cys Pro Ser Phe Asp Met
385                 390                 395                 400
```

SequenceListing

```
Thr Val Arg Asn Val Gln Thr Arg Thr Gly Arg Phe Tyr Ala Gly Val
                405                 410                 415

Gly Ser Asp Asp Asp Asn Thr Asn Thr Tyr His Leu Glu Asn Ile His
            420                 425                 430

Cys Tyr Lys Met Thr Leu Phe Gly Val Ala Thr Leu Leu Asn Met Thr
        435                 440                 445

Asn Val Thr Gly Val Val Phe Asp Ala Val Gly Asp Asp Ser Ser Gly
    450                 455                 460

Gly Thr Ser Ser Asn Gly Leu Tyr Pro Arg Lys Lys Thr Val Leu Asn
465                 470                 475                 480

Met Val Asn Val Asn Phe Tyr Gly Pro Gly Met Thr Glu Gly Ala Leu
                485                 490                 495

Tyr Ser Lys Ala Arg Tyr Ser Asp Ile Ser Thr Leu Asn Ser Asn Val
            500                 505                 510

Arg Ala Ile Pro Tyr Thr Asn Ile Gln Gly Asn Val Gly Val Ile Leu
        515                 520                 525

Ser Pro Val Asn Arg Met Tyr Thr Leu Pro Asn Ala Leu Ala Thr Leu
    530                 535                 540

Asp Gly Asn Glu Phe Pro Thr Gly Lys Glu Phe Cys Glu Gly Thr Val
545                 550                 555                 560

Leu Phe Lys Thr Asp Gly Ser Gly Gly Asn Phe Ile Val Thr Arg Phe
                565                 570                 575

Gly Ala Tyr Ile Pro Asp Asp Gly Asn Asn Phe Lys Val Arg Ala Ala
            580                 585                 590

Ala Ala Gly Gln Thr Tyr Leu Glu Gln Asn Leu Thr Pro Ala Gly Thr
        595                 600                 605

Gln Ala Ser Thr Ser Trp Leu Tyr His Lys Pro Ile Ser Ala Gly Thr
    610                 615                 620

Arg Leu Asn Val Pro Gly Ala Gly Pro Ser Gly Gly Thr Leu Thr Val
625                 630                 635                 640

Thr Val Val Arg Ala Pro Tyr Gln Val Asp Asn Asn Ile Gly Asn Pro
                645                 650                 655

Val Arg Ile Asp Ile Thr Pro Ala Ile Val Thr Ala Ile Pro Ala Gly
            660                 665                 670
```

SequenceListing

Thr Gln Leu Ala Ala Thr Tyr Pro Val Ala Tyr Ile
675 680

<210> 3
<211> 798
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence for HIS-tagged colanic acid degrading enzyme (CAE).

<400> 3

Met Gly His His His His His His Met Ala Asn Ser Tyr Asn Ala Tyr
1 5 10 15

Val Ala Asn Gly Ser Gln Thr Ala Phe Leu Val Thr Phe Glu Gln Arg
20 25 30

Val Phe Thr Glu Ile Gln Val Tyr Leu Asn Ser Glu Leu Gln Thr Glu
35 40 45

Gly Tyr Thr Tyr Asn Ser Val Thr Lys Gln Ile Ile Phe Asp Thr Ala
50 55 60

Pro Leu Ala Gly Val Ile Val Arg Leu Gln Arg Tyr Thr Ser Glu Val
65 70 75 80

Leu Leu Asn Lys Phe Gly Gln Asp Ala Ala Phe Thr Gly Gln Asn Leu
85 90 95

Asp Glu Asn Phe Glu Gln Ile Leu Phe Lys Ala Glu Glu Thr Gln Glu
100 105 110

Ala Trp Leu Ala Pro Leu Asp Arg Ala Val Arg Val Pro Asn Ser Glu
115 120 125

Val Ser Ile Asn Ala Leu Pro Asn Val Ala Gly Arg Arg Asn Lys Ala
130 135 140

Leu Gly Phe Asp Ser Asn Gly Gln Pro Phe Met Ile Pro Leu Val Asp
145 150 155 160

Ile Pro Asp Ser Ala Leu Ala Ile Ala Leu Ala Met Ala Asp Gly Gly
165 170 175

Lys Trp Ile Gly Thr Leu Gly Gly Gly Thr Phe Leu Asp Arg Gln Asp
180 185 190

Thr Val Cys Leu Ser Glu Phe Thr Asn Asn Thr Gly Tyr Ala Ser Val
195 200 205

SequenceListing

```
Ala Ala Ala Val Gln Ala Cys Phe Asp Tyr Ala Lys Ala Asn Gly Lys
    210                 215                 220

Val Val Asp Ala Arg Gly Trp Glu Gly Thr Val Asp Ser Thr Val Leu
225                 230                 235                 240

Met Asp Gly Ile Glu Val Val Gly Gly Thr Trp His Gly Lys Ala Asp
                245                 250                 255

Ile Arg Leu Leu Asn Ser Thr Phe Arg Asn Phe Val Ala Ser Thr Val
            260                 265                 270

Arg Val Ala Tyr Trp Gly Gly Glu Val Arg Ile Ala Asp Tyr Glu Phe
        275                 280                 285

Thr Ser Ala Pro Ser Asn Ser Lys Val Thr Ser Ile Leu Phe Gln Gly
    290                 295                 300

Asn Ile Ala Gly Gly Ser Tyr Val Ile Glu Asn Gly Ile His Arg Asn
305                 310                 315                 320

Gly Lys Phe Gly Ile Leu Gln Gln Gly Thr Gly Glu Ala Ile Thr Asn
                325                 330                 335

Gly Val Ile Arg Gly Ile Thr Met Met Asp Met Gln Gly Asp Gly Ile
            340                 345                 350

Glu Met Asn Val Ile Asn Lys His Tyr Asp Gly Gly Leu Leu Ile Glu
        355                 360                 365

Asn Ile Phe Leu Glu Asn Ile Asp Gly Thr Asn Ala Pro Ile Pro Leu
    370                 375                 380

Ser Asn Trp Gly Ile Gly Ile Gly Ile Ala Gly Gln Gly Pro Phe Gly
385                 390                 395                 400

Trp Asp Ala Ala Glu Thr Gln Tyr Ala Lys Asn Val Thr Val Arg Asn
                405                 410                 415

Val His Ala Pro Arg Gly Val Arg Gln Val Val His Phe Glu Val Thr
            420                 425                 430

Arg Asp Ser Thr Cys Glu Asn Val Val Ala Asn Pro Asp Leu Ser Val
        435                 440                 445

Ser Ile Gly Thr Gly Leu Thr Ala Ala Gly Val Ile Thr Tyr Gly Cys
    450                 455                 460

Lys Arg Met Thr Ile Asp Gly Val Val Gly Glu Pro Met Asn Thr Gly
465                 470                 475                 480
```

```
Ala Thr Ser Pro Asn Asp Ile Arg Ile Val Met Leu Glu Trp Gly Ala
                485                 490                 495

Asn Gln Ala Gly Ala Gly Gly Thr Pro Gly Ala Ala Cys Pro Ser Phe
            500                 505                 510

Asp Met Thr Val Arg Asn Val Gln Thr Arg Thr Gly Arg Phe Tyr Ala
        515                 520                 525

Gly Val Gly Ser Asp Asp Asp Asn Thr Asn Thr Tyr His Leu Glu Asn
    530                 535                 540

Ile His Cys Tyr Lys Met Thr Leu Phe Gly Val Ala Thr Leu Leu Asn
545                 550                 555                 560

Met Thr Asn Val Thr Gly Val Val Phe Asp Ala Val Gly Asp Asp Ser
                565                 570                 575

Ser Gly Gly Thr Ser Ser Asn Gly Leu Tyr Pro Arg Lys Lys Thr Val
            580                 585                 590

Leu Asn Met Val Asn Val Asn Phe Tyr Gly Pro Gly Met Thr Glu Gly
        595                 600                 605

Ala Leu Tyr Ser Lys Ala Arg Tyr Ser Asp Ile Ser Thr Leu Asn Ser
    610                 615                 620

Asn Val Arg Ala Ile Pro Tyr Thr Asn Ile Gln Gly Asn Val Gly Val
625                 630                 635                 640

Ile Leu Ser Pro Val Asn Arg Met Tyr Thr Leu Pro Asn Ala Leu Ala
                645                 650                 655

Thr Leu Asp Gly Asn Glu Phe Pro Thr Gly Lys Glu Phe Cys Glu Gly
            660                 665                 670

Thr Val Leu Phe Lys Thr Asp Gly Ser Gly Gly Asn Phe Ile Val Thr
        675                 680                 685

Arg Phe Gly Ala Tyr Ile Pro Asp Asp Gly Asn Asn Phe Lys Val Arg
    690                 695                 700

Ala Ala Ala Ala Gly Gln Thr Tyr Leu Glu Gln Asn Leu Thr Pro Ala
705                 710                 715                 720

Gly Thr Gln Ala Ser Thr Ser Trp Leu Tyr His Lys Pro Ile Ser Ala
                725                 730                 735

Gly Thr Arg Leu Asn Val Pro Gly Ala Gly Pro Ser Gly Gly Thr Leu
            740                 745                 750
```

SequenceListing

Thr Val Thr Val Val Arg Ala Pro Tyr Gln Val Asp Asn Asn Ile Gly
755 760 765

Asn Pro Val Arg Ile Asp Ile Thr Pro Ala Ile Val Thr Ala Ile Pro
770 775 780

Ala Gly Thr Gln Leu Ala Ala Thr Tyr Pro Val Ala Tyr Ile
785 790 795

<210> 4
<211> 692
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence for HIS-tagged truncated form of colanic acid degrading enzyme (CAE).

<400> 4

Met Gly His His His His His His Leu Ala Pro Leu Asp Arg Ala Val
1 5 10 15

Arg Val Pro Asn Ser Glu Val Ser Ile Asn Ala Leu Pro Asn Val Ala
20 25 30

Gly Arg Arg Asn Lys Ala Leu Gly Phe Asp Ser Asn Gly Gln Pro Phe
35 40 45

Met Ile Pro Leu Val Asp Ile Pro Asp Ser Ala Leu Ala Ile Ala Leu
50 55 60

Ala Met Ala Asp Gly Gly Lys Trp Ile Gly Thr Leu Gly Gly Gly Thr
65 70 75 80

Phe Leu Asp Arg Gln Asp Thr Val Cys Leu Ser Glu Phe Thr Asn Asn
85 90 95

Thr Gly Tyr Ala Ser Val Ala Ala Ala Val Gln Ala Cys Phe Asp Tyr
100 105 110

Ala Lys Ala Asn Gly Lys Val Val Asp Ala Arg Gly Trp Glu Gly Thr
115 120 125

Val Asp Ser Thr Val Leu Met Asp Gly Ile Glu Val Val Gly Gly Thr
130 135 140

Trp His Gly Lys Ala Asp Ile Arg Leu Leu Asn Ser Thr Phe Arg Asn
145 150 155 160

Phe Val Ala Ser Thr Val Arg Val Ala Tyr Trp Gly Gly Glu Val Arg
165 170 175

Ile Ala Asp Tyr Glu Phe Thr Ser Ala Pro Ser Asn Ser Lys Val Thr

180 185 190

Ser Ile Leu Phe Gln Gly Asn Ile Ala Gly Gly Ser Tyr Val Ile Glu
195 200 205

Asn Gly Ile His Arg Asn Gly Lys Phe Gly Ile Leu Gln Gln Gly Thr
210 215 220

Gly Glu Ala Ile Thr Asn Gly Val Ile Arg Gly Ile Thr Met Met Asp
225 230 235 240

Met Gln Gly Asp Gly Ile Glu Met Asn Val Ile Asn Lys His Tyr Asp
245 250 255

Gly Gly Leu Leu Ile Glu Asn Ile Phe Leu Glu Asn Ile Asp Gly Thr
260 265 270

Asn Ala Pro Ile Pro Leu Ser Asn Trp Gly Ile Gly Ile Gly Ile Ala
275 280 285

Gly Gln Gly Pro Phe Gly Trp Asp Ala Ala Glu Thr Gln Tyr Ala Lys
290 295 300

Asn Val Thr Val Arg Asn Val His Ala Pro Arg Gly Val Arg Gln Val
305 310 315 320

Val His Phe Glu Val Thr Arg Asp Ser Thr Cys Glu Asn Val Val Ala
325 330 335

Asn Pro Asp Leu Ser Val Ser Ile Gly Thr Gly Leu Thr Ala Ala Gly
340 345 350

Val Ile Thr Tyr Gly Cys Lys Arg Met Thr Ile Asp Gly Val Val Gly
355 360 365

Glu Pro Met Asn Thr Gly Ala Thr Ser Pro Asn Asp Ile Arg Ile Val
370 375 380

Met Leu Glu Trp Gly Ala Asn Gln Ala Gly Ala Gly Gly Thr Pro Gly
385 390 395 400

Ala Ala Cys Pro Ser Phe Asp Met Thr Val Arg Asn Val Gln Thr Arg
405 410 415

Thr Gly Arg Phe Tyr Ala Gly Val Gly Ser Asp Asp Asp Asn Thr Asn
420 425 430

Thr Tyr His Leu Glu Asn Ile His Cys Tyr Lys Met Thr Leu Phe Gly
435 440 445

Val Ala Thr Leu Leu Asn Met Thr Asn Val Thr Gly Val Val Phe Asp

450 455 460

Ala Val Gly Asp Asp Ser Ser Gly Gly Thr Ser Ser Asn Gly Leu Tyr
465 470 475 480

Pro Arg Lys Lys Thr Val Leu Asn Met Val Asn Val Asn Phe Tyr Gly
485 490 495

Pro Gly Met Thr Glu Gly Ala Leu Tyr Ser Lys Ala Arg Tyr Ser Asp
500 505 510

Ile Ser Thr Leu Asn Ser Asn Val Arg Ala Ile Pro Tyr Thr Asn Ile
515 520 525

Gln Gly Asn Val Gly Val Ile Leu Ser Pro Val Asn Arg Met Tyr Thr
530 535 540

Leu Pro Asn Ala Leu Ala Thr Leu Asp Gly Asn Glu Phe Pro Thr Gly
545 550 555 560

Lys Glu Phe Cys Glu Gly Thr Val Leu Phe Lys Thr Asp Gly Ser Gly
565 570 575

Gly Asn Phe Ile Val Thr Arg Phe Gly Ala Tyr Ile Pro Asp Asp Gly
580 585 590

Asn Asn Phe Lys Val Arg Ala Ala Ala Ala Gly Gln Thr Tyr Leu Glu
595 600 605

Gln Asn Leu Thr Pro Ala Gly Thr Gln Ala Ser Thr Ser Trp Leu Tyr
610 615 620

His Lys Pro Ile Ser Ala Gly Thr Arg Leu Asn Val Pro Gly Ala Gly
625 630 635 640

Pro Ser Gly Gly Thr Leu Thr Val Thr Val Val Arg Ala Pro Tyr Gln
645 650 655

Val Asp Asn Asn Ile Gly Asn Pro Val Arg Ile Asp Ile Thr Pro Ala
660 665 670

Ile Val Thr Ala Ile Pro Ala Gly Thr Gln Leu Ala Ala Thr Tyr Pro
675 680 685

Val Ala Tyr Ile
690

<210> 5
<211> 798
<212> PRT
<213> Artificial

SequenceListing

<220>
<223> Amino acid sequence for FLAG-tagged colanic acid degrading enzyme (CAE).

<400> 5

```
Met Ala Asn Ser Tyr Asn Ala Tyr Val Ala Asn Gly Ser Gln Thr Ala
1               5                  10                  15

Phe Leu Val Thr Phe Glu Gln Arg Val Phe Thr Glu Ile Gln Val Tyr
            20                  25                  30

Leu Asn Ser Glu Leu Gln Thr Glu Gly Tyr Thr Tyr Asn Ser Val Thr
        35                  40                  45

Lys Gln Ile Ile Phe Asp Thr Ala Pro Leu Ala Gly Val Ile Val Arg
    50                  55                  60

Leu Gln Arg Tyr Thr Ser Glu Val Leu Leu Asn Lys Phe Gly Gln Asp
65                  70                  75                  80

Ala Ala Phe Thr Gly Gln Asn Leu Asp Glu Asn Phe Glu Gln Ile Leu
                85                  90                  95

Phe Lys Ala Glu Glu Thr Gln Glu Ala Trp Leu Ala Pro Leu Asp Arg
            100                 105                 110

Ala Val Arg Val Pro Asn Ser Glu Val Ser Ile Asn Ala Leu Pro Asn
        115                 120                 125

Val Ala Gly Arg Arg Asn Lys Ala Leu Gly Phe Asp Ser Asn Gly Gln
    130                 135                 140

Pro Phe Met Ile Pro Leu Val Asp Ile Pro Asp Ser Ala Leu Ala Ile
145                 150                 155                 160

Ala Leu Ala Met Ala Asp Gly Gly Lys Trp Ile Gly Thr Leu Gly Gly
                165                 170                 175

Gly Thr Phe Leu Asp Arg Gln Asp Thr Val Cys Leu Ser Glu Phe Thr
            180                 185                 190

Asn Asn Thr Gly Tyr Ala Ser Val Ala Ala Ala Val Gln Ala Cys Phe
        195                 200                 205

Asp Tyr Ala Lys Ala Asn Gly Lys Val Val Asp Ala Arg Gly Trp Glu
    210                 215                 220

Gly Thr Val Asp Ser Thr Val Leu Met Asp Gly Ile Glu Val Val Gly
225                 230                 235                 240

Gly Thr Trp His Gly Lys Ala Asp Ile Arg Leu Leu Asn Ser Thr Phe
                245                 250                 255
```

SequenceListing

```
Arg Asn Phe Val Ala Ser Thr Val Arg Val Ala Tyr Trp Gly Gly Glu
            260                 265                 270

Val Arg Ile Ala Asp Tyr Glu Phe Thr Ser Ala Pro Ser Asn Ser Lys
        275                 280                 285

Val Thr Ser Ile Leu Phe Gln Gly Asn Ile Ala Gly Gly Ser Tyr Val
    290                 295                 300

Ile Glu Asn Gly Ile His Arg Asn Gly Lys Phe Gly Ile Leu Gln Gln
305                 310                 315                 320

Gly Thr Gly Glu Ala Ile Thr Asn Gly Val Ile Arg Gly Ile Thr Met
                325                 330                 335

Met Asp Met Gln Gly Asp Gly Ile Glu Met Asn Val Ile Asn Lys His
            340                 345                 350

Tyr Asp Gly Gly Leu Leu Ile Glu Asn Ile Phe Leu Glu Asn Ile Asp
        355                 360                 365

Gly Thr Asn Ala Pro Ile Pro Leu Ser Asn Trp Gly Ile Gly Ile Gly
    370                 375                 380

Ile Ala Gly Gln Gly Pro Phe Gly Trp Asp Ala Ala Glu Thr Gln Tyr
385                 390                 395                 400

Ala Lys Asn Val Thr Val Arg Asn Val His Ala Pro Arg Gly Val Arg
                405                 410                 415

Gln Val Val His Phe Glu Val Thr Arg Asp Ser Thr Cys Glu Asn Val
            420                 425                 430

Val Ala Asn Pro Asp Leu Ser Val Ser Ile Gly Thr Gly Leu Thr Ala
        435                 440                 445

Ala Gly Val Ile Thr Tyr Gly Cys Lys Arg Met Thr Ile Asp Gly Val
    450                 455                 460

Val Gly Glu Pro Met Asn Thr Gly Ala Thr Ser Pro Asn Asp Ile Arg
465                 470                 475                 480

Ile Val Met Leu Glu Trp Gly Ala Asn Gln Ala Gly Ala Gly Gly Thr
                485                 490                 495

Pro Gly Ala Ala Cys Pro Ser Phe Asp Met Thr Val Arg Asn Val Gln
            500                 505                 510

Thr Arg Thr Gly Arg Phe Tyr Ala Gly Val Gly Ser Asp Asp Asp Asn
        515                 520                 525
```

SequenceListing

```
Thr Asn Thr Tyr His Leu Glu Asn Ile His Cys Tyr Lys Met Thr Leu
    530                 535                 540

Phe Gly Val Ala Thr Leu Leu Asn Met Thr Asn Val Thr Gly Val Val
545                 550                 555                 560

Phe Asp Ala Val Gly Asp Asp Ser Ser Gly Gly Thr Ser Ser Asn Gly
                565                 570                 575

Leu Tyr Pro Arg Lys Lys Thr Val Leu Asn Met Val Asn Val Asn Phe
            580                 585                 590

Tyr Gly Pro Gly Met Thr Glu Gly Ala Leu Tyr Ser Lys Ala Arg Tyr
        595                 600                 605

Ser Asp Ile Ser Thr Leu Asn Ser Asn Val Arg Ala Ile Pro Tyr Thr
    610                 615                 620

Asn Ile Gln Gly Asn Val Gly Val Ile Leu Ser Pro Val Asn Arg Met
625                 630                 635                 640

Tyr Thr Leu Pro Asn Ala Leu Ala Thr Leu Asp Gly Asn Glu Phe Pro
                645                 650                 655

Thr Gly Lys Glu Phe Cys Glu Gly Thr Val Leu Phe Lys Thr Asp Gly
            660                 665                 670

Ser Gly Gly Asn Phe Ile Val Thr Arg Phe Gly Ala Tyr Ile Pro Asp
        675                 680                 685

Asp Gly Asn Asn Phe Lys Val Arg Ala Ala Ala Ala Gly Gln Thr Tyr
    690                 695                 700

Leu Glu Gln Asn Leu Thr Pro Ala Gly Thr Gln Ala Ser Thr Ser Trp
705                 710                 715                 720

Leu Tyr His Lys Pro Ile Ser Ala Gly Thr Arg Leu Asn Val Pro Gly
                725                 730                 735

Ala Gly Pro Ser Gly Gly Thr Leu Thr Val Thr Val Val Arg Ala Pro
            740                 745                 750

Tyr Gln Val Asp Asn Asn Ile Gly Asn Pro Val Arg Ile Asp Ile Thr
        755                 760                 765

Pro Ala Ile Val Thr Ala Ile Pro Ala Gly Thr Gln Leu Ala Ala Thr
    770                 775                 780

Tyr Pro Val Ala Tyr Ile Asp Tyr Lys Asp Asp Asp Asp Lys
785                 790                 795
```

SequenceListing

<210> 6
<211> 692
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence for FLAG-tagged truncated form of colanic acid degrading enzyme (CAE).

<400> 6

```
Leu Ala Pro Leu Asp Arg Ala Val Arg Val Pro Asn Ser Glu Val Ser
1               5                   10                  15

Ile Asn Ala Leu Pro Asn Val Ala Gly Arg Arg Asn Lys Ala Leu Gly
            20                  25                  30

Phe Asp Ser Asn Gly Gln Pro Phe Met Ile Pro Leu Val Asp Ile Pro
        35                  40                  45

Asp Ser Ala Leu Ala Ile Ala Leu Ala Met Ala Asp Gly Gly Lys Trp
    50                  55                  60

Ile Gly Thr Leu Gly Gly Gly Thr Phe Leu Asp Arg Gln Asp Thr Val
65                  70                  75                  80

Cys Leu Ser Glu Phe Thr Asn Asn Thr Gly Tyr Ala Ser Val Ala Ala
                85                  90                  95

Ala Val Gln Ala Cys Phe Asp Tyr Ala Lys Ala Asn Gly Lys Val Val
            100                 105                 110

Asp Ala Arg Gly Trp Glu Gly Thr Val Asp Ser Thr Val Leu Met Asp
        115                 120                 125

Gly Ile Glu Val Val Gly Gly Thr Trp His Gly Lys Ala Asp Ile Arg
    130                 135                 140

Leu Leu Asn Ser Thr Phe Arg Asn Phe Val Ala Ser Thr Val Arg Val
145                 150                 155                 160

Ala Tyr Trp Gly Gly Glu Val Arg Ile Ala Asp Tyr Glu Phe Thr Ser
                165                 170                 175

Ala Pro Ser Asn Ser Lys Val Thr Ser Ile Leu Phe Gln Gly Asn Ile
            180                 185                 190

Ala Gly Gly Ser Tyr Val Ile Glu Asn Gly Ile His Arg Asn Gly Lys
        195                 200                 205

Phe Gly Ile Leu Gln Gln Gly Thr Gly Glu Ala Ile Thr Asn Gly Val
    210                 215                 220
```

SequenceListing

```
Ile Arg Gly Ile Thr Met Met Asp Met Gln Gly Asp Gly Ile Glu Met
225                 230                 235                 240

Asn Val Ile Asn Lys His Tyr Asp Gly Gly Leu Leu Ile Glu Asn Ile
                245                 250                 255

Phe Leu Glu Asn Ile Asp Gly Thr Asn Ala Pro Ile Pro Leu Ser Asn
            260                 265                 270

Trp Gly Ile Gly Ile Gly Ile Ala Gly Gln Gly Pro Phe Gly Trp Asp
        275                 280                 285

Ala Ala Glu Thr Gln Tyr Ala Lys Asn Val Thr Val Arg Asn Val His
    290                 295                 300

Ala Pro Arg Gly Val Arg Gln Val Val His Phe Glu Val Thr Arg Asp
305                 310                 315                 320

Ser Thr Cys Glu Asn Val Val Ala Asn Pro Asp Leu Ser Val Ser Ile
                325                 330                 335

Gly Thr Gly Leu Thr Ala Ala Gly Val Ile Thr Tyr Gly Cys Lys Arg
            340                 345                 350

Met Thr Ile Asp Gly Val Val Gly Glu Pro Met Asn Thr Gly Ala Thr
        355                 360                 365

Ser Pro Asn Asp Ile Arg Ile Val Met Leu Glu Trp Gly Ala Asn Gln
    370                 375                 380

Ala Gly Ala Gly Gly Thr Pro Gly Ala Ala Cys Pro Ser Phe Asp Met
385                 390                 395                 400

Thr Val Arg Asn Val Gln Thr Arg Thr Gly Arg Phe Tyr Ala Gly Val
                405                 410                 415

Gly Ser Asp Asp Asp Asn Thr Asn Thr Tyr His Leu Glu Asn Ile His
            420                 425                 430

Cys Tyr Lys Met Thr Leu Phe Gly Val Ala Thr Leu Leu Asn Met Thr
        435                 440                 445

Asn Val Thr Gly Val Val Phe Asp Ala Val Gly Asp Asp Ser Ser Gly
    450                 455                 460

Gly Thr Ser Ser Asn Gly Leu Tyr Pro Arg Lys Lys Thr Val Leu Asn
465                 470                 475                 480

Met Val Asn Val Asn Phe Tyr Gly Pro Gly Met Thr Glu Gly Ala Leu
                485                 490                 495
```

SequenceListing

```
Tyr Ser Lys Ala Arg Tyr Ser Asp Ile Ser Thr Leu Asn Ser Asn Val
            500                 505                 510

Arg Ala Ile Pro Tyr Thr Asn Ile Gln Gly Asn Val Gly Val Ile Leu
        515                 520                 525

Ser Pro Val Asn Arg Met Tyr Thr Leu Pro Asn Ala Leu Ala Thr Leu
    530                 535                 540

Asp Gly Asn Glu Phe Pro Thr Gly Lys Glu Phe Cys Glu Gly Thr Val
545                 550                 555                 560

Leu Phe Lys Thr Asp Gly Ser Gly Gly Asn Phe Ile Val Thr Arg Phe
                565                 570                 575

Gly Ala Tyr Ile Pro Asp Asp Gly Asn Asn Phe Lys Val Arg Ala Ala
            580                 585                 590

Ala Ala Gly Gln Thr Tyr Leu Glu Gln Asn Leu Thr Pro Ala Gly Thr
        595                 600                 605

Gln Ala Ser Thr Ser Trp Leu Tyr His Lys Pro Ile Ser Ala Gly Thr
    610                 615                 620

Arg Leu Asn Val Pro Gly Ala Gly Pro Ser Gly Gly Thr Leu Thr Val
625                 630                 635                 640

Thr Val Val Arg Ala Pro Tyr Gln Val Asp Asn Asn Ile Gly Asn Pro
                645                 650                 655

Val Arg Ile Asp Ile Thr Pro Ala Ile Val Thr Ala Ile Pro Ala Gly
            660                 665                 670

Thr Gln Leu Ala Ala Thr Tyr Pro Val Ala Tyr Ile Asp Tyr Lys Asp
        675                 680                 685

Asp Asp Asp Lys
    690
```

<210> 7
<211> 2373
<212> DNA
<213> Artificial

<220>
<223> Nucleic acid sequence encoding a colanic acid degrading enzyme (CAE).

<400> 7

```
atggcgaaca gctataatgc ttacgtggcg aacggttcac agaccgcatt cctcgtcacg     60

ttcgagcagc gcgtgttcac tgagattcag gtgtacctca actccgaact ccagacggaa    120

gggtacacct acaactctgt gaccaaacag attatcttcg acaccgcccc gctcgccggg    180
```

SequenceListing

gtgattgtcc gactccaacg ctacacctct gaggttctgc tgaacaagtt tggccaagac 240
gctgccttca ccgggcagaa ccttgacgag aactttgagc agattctgtt caaggctgag 300
gaaactcagg aagcatggct cgcgccactt gaccgcgccg tccgtgttcc gaactccgaa 360
gtctccatca acgcattacc gaacgtcgct ggccgccgca acaaggcact gggctttgac 420
agcaatggtc agccgttcat gattcctctg gtcgatatcc cggactccgc gctggcgatt 480
gctctggcaa tggctgacgg cggtaagtgg attggtactc tcggcggggg cacgttcctc 540
gaccgtcagg ataccgtctg cctgtccgag ttcaccaaca acactgggta cgcctctgtc 600
gccgctgcgg tgcaggcttg cttcgactat gcgaaagcca acggcaaggt cgttgacgct 660
cgcggctggg aaggtacggt ggattccact gtgctgatgg acggtattga ggtcgtcggc 720
ggtacgtggc acggcaaggc tgacattcgc ctgctgaact ccaccttccg caacttcgtg 780
gcctctactg tccgtgtcgc ctactggggc ggcgaggtgc gtattgctga ctatgagttc 840
accagcgcac cgagcaactc caaggttacg tctatcctgt tccaaggcaa catcgccggg 900
ggcagctacg tcattgagaa cggtatccac cgcaatggta agttcggtat tctccaacag 960
ggtactggcg aggctatcac caacggcgtt atccgtggca tcaccatgat ggatatgcag 1020
ggtgacggta tcgagatgaa cgtaatcaac aagcactatg atggtggcct gctgattgag 1080
aacatcttcc ttgagaacat cgacggcacc aacgcgccta tcccactgtc caactggggc 1140
attggtatcg gtatcgctgg tcaaggcccg ttcggttggg atgctgctga gacgcagtat 1200
gcgaagaacg tcactgtccg taacgtccat gctccgcgtg gtgtgcgtca ggtcgtccac 1260
ttcgaggtta cgcgtgacag cacctgcgag aacgtagtgg ccaaccctga cctgtccgtc 1320
tccattggta ctggcctgac tgccgctggt gtaatcacgt acggctgcaa gcgcatgacc 1380
attgacggtg tagtcggtga gcctatgaac accggagcaa cctctccgaa cgatattcgt 1440
atcgtgatgt tggagtgggg tgcgaaccaa gcaggtgctg gcggtacgcc gggtgcagct 1500
tgcccatcgt tcgacatgac cgtgcgtaac gtgcagaccc gtaccgggcg cttctatgct 1560
ggtgtcggct ccgacgatga caacaccaac acatatcacc ttgaaaacat tcactgttac 1620
aagatgacgc tgtttggtgt ggcaactctg ctgaacatga ccaacgtgac tggtgtggtg 1680
ttcgacgctg taggcgatga ctccagcggc ggtacgtcct ccaacggtct gtacccgcgt 1740
aagaagactg ttctcaacat ggtgaacgtg aacttctacg ggccgggcat gaccgagggt 1800
gcgctgtaca gtaaggctcg ctactcggat atcagcacgc tgaactccaa cgtgcgtgct 1860
atcccgtaca ccaacatcca aggtaacgtg ggtgtcatcc tgtctccggt caaccgcatg 1920
tacacgctgc cgaacgccct cgctaccctt gacggtaatg agttccccac cgggaaagag 1980
ttctgcgaag gtactgtgct gttcaagacc gatggctccg gtggcaactt catcgtgacc 2040
cggttcggtg cgtacatccc ggatgacggt aacaacttca aggtgcgtgc tgctgccgct 2100
ggccagacgt atctggagca gaacctgact ccggctggta ctcaggcttc cacctcgtgg 2160
ctgtaccata agccaatctc tgctggtact cgactcaatg ttccgggtgc cgggccgagc 2220

SequenceListing

ggcggtacgc tcactgtgac ggtggtgcgt gctccgtatc aggtggacaa caacatcgga 2280

aacccggtac gcatcgacat taccccggcc attgtgacgg caatccctgc gggaacgcag 2340

ctcgccgcta cctacccggt ggcttacatc taa 2373

<210> 8
<211> 2055
<212> DNA
<213> Artificial

<220>
<223> Nucleic acid sequence encoding a truncated form of a colanic acid degrading enzyme (CAE).

<400> 8
ctcgcgccac ttgaccgcgc cgtccgtgtt ccgaactccg aagtctccat caacgcatta 60

ccgaacgtcg ctggccgccg caacaaggca ctgggctttg acagcaatgg tcagccgttc 120

atgattcctc tggtcgatat cccggactcc gcgctggcga ttgctctggc aatggctgac 180

ggcggtaagt ggattggtac tctcggcggg ggcacgttcc tcgaccgtca ggataccgtc 240

tgcctgtccg agttcaccaa caacactggg tacgcctctg tcgccgctgc ggtgcaggct 300

tgcttcgact atgcgaaagc caacggcaag gtcgttgacg ctcgcggctg ggaaggtacg 360

gtggattcca ctgtgctgat ggacggtatt gaggtcgtcg gcggtacgtg gcacggcaag 420

gctgacattc gcctgctgaa ctccaccttc cgcaacttcg tggcctctac tgtccgtgtc 480

gcctactggg gcggcgaggt gcgtattgct gactatgagt tcaccagcgc accgagcaac 540

tccaaggtta cgtctatcct gttccaaggc aacatcgccg ggggcagcta cgtcattgag 600

aacggtatcc accgcaatgg taagttcggt attctccaac agggtactgg cgaggctatc 660

accaacggcg ttatccgtgg catcaccatg atggatatgc agggtgacgg tatcgagatg 720

aacgtaatca acaagcacta tgatggtggc ctgctgattg agaacatctt ccttgagaac 780

atcgacggca ccaacgcgcc tatcccactg tccaactggg gcattggtat cggtatcgct 840

ggtcaaggcc cgttcggttg ggatgctgct gagacgcagt atgcgaagaa cgtcactgtc 900

cgtaacgtcc atgctccgcg tggtgtgcgt caggtcgtcc acttcgaggt tacgcgtgac 960

agcacctgcg agaacgtagt ggccaaccct gacctgtccg tctccattgg tactggcctg 1020

actgccgctg gtgtaatcac gtacggctgc aagcgcatga ccattgacgg tgtagtcggt 1080

gagcctatga acaccggagc aacctctccg aacgatattc gtatcgtgat gttggagtgg 1140

ggtgcgaacc aagcaggtgc tggcggtacg ccgggtgcag cttgcccatc gttcgacatg 1200

accgtgcgta acgtgcagac ccgtaccggg cgcttctatg ctggtgtcgg ctccgacgat 1260

gacaacacca acacatatca ccttgaaaac attcactgtt acaagatgac gctgtttggt 1320

gtggcaactc tgctgaacat gaccaacgtg actggtgtgg tgttcgacgc tgtaggcgat 1380

gactccagcg gcggtacgtc ctccaacggt ctgtacccgc gtaagaagac tgttctcaac 1440

atggtgaacg tgaacttcta cgggccgggc atgaccgagg gtgcgctgta cagtaaggct 1500

SequenceListing

cgctactcgg atatcagcac gctgaactcc aacgtgcgtg ctatcccgta caccaacatc 1560

caaggtaacg tgggtgtcat cctgtctccg gtcaaccgca tgtacacgct gccgaacgcc 1620

ctcgctaccc ttgacggtaa tgagttcccc accgggaaag agttctgcga aggtactgtg 1680

ctgttcaaga ccgatggctc cggtggcaac ttcatcgtga cccggttcgg tgcgtacatc 1740

ccggatgacg gtaacaactt caaggtgcgt gctgctgccg ctggccagac gtatctggag 1800

cagaacctga ctccggctgg tactcaggct tccacctcgt ggctgtacca taagccaatc 1860

tctgctggta ctcgactcaa tgttccgggt gccgggccga gcggcggtac gctcactgtg 1920

acggtggtgc gtgctccgta tcaggtggac aacaacatcg gaaacccggt acgcatcgac 1980

attaccccgg ccattgtgac ggcaatccct gcgggaacgc agctcgccgc tacctacccg 2040

gtggcttaca tctaa 2055

<210> 9
<211> 15
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of a colanic acid degrading enzyme (CAE) fragment.

<400> 9

Ala Asn Ser Tyr Asn Ala Tyr Val Ala Asn Gly Ser Gln Thr Ala
1 5 10 15

<210> 10
<211> 16
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of a colanic acid degrading enzyme (CAE) fragment.

<400> 10

Leu Leu Glu Gln Gly Thr Gly Glu Ala Leu Thr Asp Gly Val Leu Arg
1 5 10 15

<210> 11
<211> 16
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of a colanic acid degrading enzyme (CAE) fragment.

<400> 11

Val Pro Asn Ser Glu Val Ser Leu Asn Ala Leu Pro Asn Val Gln Arg
1 5 10 15

<210> 12
<211> 14

SequenceListing

<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of a colanic acid degrading enzyme (CAE) fragment.

<400> 12

Leu Ala Asp Tyr Glu Phe Thr Ser Ala Pro Ser Asn Ser Lys
1 5 10

<210> 13
<211> 8
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of a colanic acid degrading enzyme (CAE) fragment.

<400> 13

Tyr Ser Asp Leu Ser Thr Leu Asn
1 5

<210> 14
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of a colanic acid degrading enzyme (CAE) fragment.

<400> 14

Gln Leu Leu Phe Asp Thr Ala Pro Leu Ala
1 5 10

<210> 15
<211> 9
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of a colanic acid degrading enzyme (CAE) fragment.

<400> 15

Ala Pro Tyr Gln Val Asp Asp Asn Leu
1 5

<210> 16
<211> 8
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of a colanic acid degrading enzyme (CAE) fragment.

<400> 16

SequenceListing

Phe Gly Ala Tyr Leu Pro Asp Asp
1 5

<210> 17
<211> 6
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of a colanic acid degrading enzyme (CAE) fragment.

<400> 17

Leu Gly Thr Leu Gly Gly
1 5